

SEQUENCE LISTING

<110> Unitectra Inc.

<120> Pharmaceutical Compositions for Treating or Preventing Cancer

<130> E 2862 EP

<140>

<141>

<160> 13

<170> PatentIn Ver. 2.1

<210> 1

<211> 1881

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(1881)

<400> 1

atg	gtg	ggt	gtc	cag	aga	agg	agc	ttc	ctt	ccc	gtg	ctt	gtg	ctg	agt	48
Met	Val	Gly	Val	Gln	Arg	Arg	Ser	Phe	Leu	Pro	Val	Leu	Val	Leu	Ser	
1				5					10					15		

gct	ctg	ctg	gct	gtg	ggg	gcc	cta	gaa	gga	tcc	agg	aat	cag	gac	tgg	96
Ala	Leu	Leu	Ala	Val	Gly	Ala	Leu	Glu	Gly	Ser	Arg	Asn	Gln	Asp	Trp	
			20					25						30		

ctt	ggt	gtc	cca	aga	caa	ctt	gta	act	aaa	acc	tgg	aac	agg	cag	ctg	144
Leu	Gly	Val	Pro	Arg	Gln	Leu	Val	Thr	Lys	Thr	Trp	Asn	Arg	Gln	Leu	
		35					40						45			

tac	ccc	gag	tgg	aca	gag	gtg	cag	ggg	tct	aac	tgc	tgg	aga	ggt	ggc	192
Tyr	Pro	Glu	Trp	Thr	Glu	Val	Gln	Gly	Ser	Asn	Cys	Trp	Arg	Gly	Gly	
		50				55					60					

cag	gta	tct	ctg	agg	gtc	att	aat	gat	ggg	cct	aca	ctg	gtt	ggt	gca	240
Gln	Val	Ser	Leu	Arg	Val	Ile	Asn	Asp	Gly	Pro	Thr	Leu	Val	Gly	Ala	
	65				70				75					80		

aat	gcc	tcc	ttt	tcc	att	gcc	ctg	cac	ttc	cct	gga	agt	caa	aag	gta	288
Asn	Ala	Ser	Phe	Ser	Ile	Ala	Leu	His	Phe	Pro	Gly	Ser	Gln	Lys	Val	
			85						90					95		

cta	ccg	gat	ggt	cag	gtt	atc	tgg	gcc	aac	aac	acc	atc	atc	aat	ggg	336
Leu	Pro	Asp	Gly	Gln	Val	Ile	Trp	Ala	Asn	Asn	Thr	Ile	Ile	Asn	Gly	
			100					105						110		

agc	cag	gtg	tgg	gga	gga	cag	cca	gtg	tat	cca	cag	gag	cct	gat	gat	384
Ser	Gln	Val	Trp	Gly	Gly	Gln	Pro	Val	Tyr	Pro	Gln	Glu	Pro	Asp	Asp	
		115						120					125			

gcc	tgt	gtc	ttc	cct	gac	ggt	gga	ccc	tgc	cca	tct	ggt	cct	aaa	cct	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1047533 041502

Ala Cys Val Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Pro Lys Pro	
130 135 140	
ccg aag aga agc ttt gtt tat gtt tgg aag acc tgg gga aaa tac tgg	480
Pro Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Lys Tyr Trp	
145 150 155 160	
caa gtt ctg ggg ggt cca gtg tcc agg tcg agc att gct acg cgc cac	528
Gln Val Leu Gly Gly Pro Val Ser Arg Ser Ser Ile Ala Thr Arg His	
165 170 175	
gca aag ctg ggc aca cac aca atg gaa gtg act gtc tac cac cga cgg	576
Ala Lys Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg	
180 185 190	
ggc tcc cag agc tac gtg ccc ctt gct cac gcc agt tca acc ttc acc	624
Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ala Ser Ser Thr Phe Thr	
195 200 205	
att act gac cag gta cct ttc tcc gtg agt gtg tcc cag cta cag gcc	672
Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala	
210 215 220	
ttg gac gga gag acc aag cac ttc ctg aga aat cat cct ctc atc ttt	720
Leu Asp Gly Glu Thr Lys His Phe Leu Arg Asn His Pro Leu Ile Phe	
225 230 235 240	
gcc ctt cag ctc cac gac ccc agt ggt tat ttg gcc gag gcc gac ctc	768
Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu	
245 250 255	
tcc tac aca tgg gac ttt gga gat ggt act ggg acc ctg atc tct cgg	816
Ser Tyr Thr Trp Asp Phe Gly Asp Gly Thr Gly Thr Leu Ile Ser Arg	
260 265 270	
gca ctt gat gtc act cac act tac ctg gag tcg ggc tca gtc act gcc	864
Ala Leu Asp Val Thr His Thr Tyr Leu Glu Ser Gly Ser Val Thr Ala	
275 280 285	
cag gtg gta ctg cag gct gcc att cct ctt gtt tcc tgt ggt tcc tcc	912
Gln Val Val Leu Gln Ala Ala Ile Pro Leu Val Ser Cys Gly Ser Ser	
290 295 300	
cca gtc ccg ggt acc aca gat ggc tac atg cca act gca gaa gca cct	960
Pro Val Pro Gly Thr Thr Asp Gly Tyr Met Pro Thr Ala Glu Ala Pro	
305 310 315 320	
gga acc aca tct agg caa gga acc act aca aaa gtt gtg ggt act aca	1008
Gly Thr Thr Ser Arg Gln Gly Thr Thr Thr Lys Val Val Gly Thr Thr	
325 330 335	
cct ggc cag atg cca act aca cag ccc tct gga acc aca gtt gta caa	1056
Pro Gly Gln Met Pro Thr Thr Gln Pro Ser Gly Thr Thr Val Val Gln	
340 345 350	
atg cca acc aca gag gtc aca gct act aca tct gag cag atg ctg acc	1104
Met Pro Thr Thr Glu Val Thr Ala Thr Thr Ser Glu Gln Met Leu Thr	
355 360 365	

tca gcg gtc ata gat acc aca ctg gca gag gtg tca act aca gag ggt 1152
 Ser Ala Val Ile Asp Thr Thr Leu Ala Glu Val Ser Thr Thr Glu Gly
 370 375 380

aca ggt acc aca ccc aca agg cct tct gga acc acc gtt gca caa gca 1200
 Thr Gly Thr Thr Pro Thr Arg Pro Ser Gly Thr Thr Val Ala Gln Ala
 385 390 395 400

aca acc aca gag ggt cca gat gcc agc cca ttg ctg ccc aca caa agt 1248
 Thr Thr Thr Glu Gly Pro Asp Ala Ser Pro Leu Leu Pro Thr Gln Ser
 405 410 415

tct aca ggg tcc att agc cct cta ctg gat gac acc gac acc ata atg 1296
 Ser Thr Gly Ser Ile Ser Pro Leu Leu Asp Asp Thr Asp Thr Ile Met
 420 425 430

ctt gtg aag aga caa gtt ccc ctg gac tgt gtt cta tat cga tat ggt 1344
 Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr Gly
 435 440 445

tct ttc tcc ctg gcc ctg gac att gtc cag ggt att gaa agt gct gag 1392
 Ser Phe Ser Leu Ala Leu Asp Ile Val Gln Gly Ile Glu Ser Ala Glu
 450 455 460

atc ctg cag gct gtg cca ttc agt gaa ggg gat gca ttt gag ctg act 1440
 Ile Leu Gln Ala Val Pro Phe Ser Glu Gly Asp Ala Phe Glu Leu Thr
 465 470 475 480

gtg tcc tgc caa ggc ggg cta ccc aag gaa gcc tgt atg gac att tca 1488
 Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Asp Ile Ser
 485 490 495

tca cca ggg tgc cag ccc cct gcc cag agg ctg tgc cag tct gtt cca 1536
 Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Ser Val Pro
 500 505 510

ccg agc cca gac tgc cag ctg gtt cta cac caa gtg ctg aaa ggt ggc 1584
 Pro Ser Pro Asp Cys Gln Leu Val Leu His Gln Val Leu Lys Gly Gly
 515 520 525

tca ggg aca tat tgc ctg aat gtg tct ttg gct gac gcc aac agc ctg 1632
 Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala Asn Ser Leu
 530 535 540

gca gtg gcc agc acc caa ctt gtt gtt cct ggt caa gac ggt ggc ctt 1680
 Ala Val Ala Ser Thr Gln Leu Val Val Pro Gly Gln Asp Gly Gly Leu
 545 550 555 560

ggg cag gct ccc ttg ctt gta ggt atc ttg ctg gtg ttg gtg gct gtg 1728
 Gly Gln Ala Pro Leu Leu Val Gly Ile Leu Leu Val Leu Val Ala Val
 565 570 575

gtc ctt gca tct ctg ata cta ggc ata gac tta aga agc agg gct cag 1776
 Val Leu Ala Ser Leu Ile Leu Gly Ile Asp Leu Arg Ser Arg Ala Gln
 580 585 590

ttt ccc aaa tgc cac atg gta gca ctg act gct gcg cct gcc tcc ggt 1824
 Phe Pro Lys Cys His Met Val Ala Leu Thr Ala Ala Pro Ala Ser Gly
 595 600 605

10047539.01502

ctt cgc gcc cgc ggc ctt gga gaa aac agc ccg ctc ctc agt gga cag 1872
 Leu Arg Ala Arg Gly Leu Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln
 610 615 620

cag gtc tga 1881
 Gln Val
 625

<210> 2
 <211> 626
 <212> PRT
 <213> Mus musculus

<400> 2
 Met Val Gly Val Gln Arg Arg Ser Phe Leu Pro Val Leu Val Leu Ser
 1 5 10 15

Ala Leu Leu Ala Val Gly Ala Leu Glu Gly Ser Arg Asn Gln Asp Trp
 20 25 30

Leu Gly Val Pro Arg Gln Leu Val Thr Lys Thr Trp Asn Arg Gln Leu
 35 40 45

Tyr Pro Glu Trp Thr Glu Val Gln Gly Ser Asn Cys Trp Arg Gly Gly
 50 55 60

Gln Val Ser Leu Arg Val Ile Asn Asp Gly Pro Thr Leu Val Gly Ala
 65 70 75 80

Asn Ala Ser Phe Ser Ile Ala Leu His Phe Pro Gly Ser Gln Lys Val
 85 90 95

Leu Pro Asp Gly Gln Val Ile Trp Ala Asn Asn Thr Ile Ile Asn Gly
 100 105 110

Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Pro Asp Asp
 115 120 125

Ala Cys Val Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Pro Lys Pro
 130 135 140

Pro Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Lys Tyr Trp
 145 150 155 160

Gln Val Leu Gly Gly Pro Val Ser Arg Ser Ser Ile Ala Thr Arg His
 165 170 175

Ala Lys Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
 180 185 190

Gly Ser Gln Ser Tyr Val Pro Leu Ala His Ala Ser Ser Thr Phe Thr
 195 200 205

Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Gln Ala
 210 215 220

Leu Asp Gly Glu Thr Lys His Phe Leu Arg Asn His Pro Leu Ile Phe

202510" 6554001

225	230	235	240
Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu	245	250	255
Ser Tyr Thr Trp Asp Phe Gly Asp Gly Thr Gly Thr Leu Ile Ser Arg	260	265	270
Ala Leu Asp Val Thr His Thr Tyr Leu Glu Ser Gly Ser Val Thr Ala	275	280	285
Gln Val Val Leu Gln Ala Ala Ile Pro Leu Val Ser Cys Gly Ser Ser	290	295	300
Pro Val Pro Gly Thr Thr Asp Gly Tyr Met Pro Thr Ala Glu Ala Pro	305	310	315
Gly Thr Thr Ser Arg Gln Gly Thr Thr Thr Lys Val Val Gly Thr Thr	325	330	335
Pro Gly Gln Met Pro Thr Thr Gln Pro Ser Gly Thr Thr Val Val Gln	340	345	350
Met Pro Thr Thr Glu Val Thr Ala Thr Thr Ser Glu Gln Met Leu Thr	355	360	365
Ser Ala Val Ile Asp Thr Thr Leu Ala Glu Val Ser Thr Thr Glu Gly	370	375	380
Thr Gly Thr Thr Pro Thr Arg Pro Ser Gly Thr Thr Val Ala Gln Ala	385	390	395
Thr Thr Thr Glu Gly Pro Asp Ala Ser Pro Leu Leu Pro Thr Gln Ser	405	410	415
Ser Thr Gly Ser Ile Ser Pro Leu Leu Asp Asp Thr Asp Thr Ile Met	420	425	430
Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr Gly	435	440	445
Ser Phe Ser Leu Ala Leu Asp Ile Val Gln Gly Ile Glu Ser Ala Glu	450	455	460
Ile Leu Gln Ala Val Pro Phe Ser Glu Gly Asp Ala Phe Glu Leu Thr	465	470	475
Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Asp Ile Ser	485	490	495
Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Ser Val Pro	500	505	510
Pro Ser Pro Asp Cys Gln Leu Val Leu His Gln Val Leu Lys Gly Gly	515	520	525
Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Ala Asn Ser Leu	530	535	540

Ala Val Ala Ser Thr Gln Leu Val Val Pro Gly Gln Asp Gly Gly Leu
545 550 555 560

Gly Gln Ala Pro Leu Leu Val Gly Ile Leu Leu Val Leu Val Ala Val
565 570 575

Val Leu Ala Ser Leu Ile Leu Gly Ile Asp Leu Arg Ser Arg Ala Gln
580 585 590

Phe Pro Lys Cys His Met Val Ala Leu Thr Ala Ala Pro Ala Ser Gly
595 600 605

Leu Arg Ala Arg Gly Leu Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln
610 615 620

Gln Val
625

<210> 3
<211> 2131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (12)..(2018)

<400> 3
ggaagaacac a atg gat ctg gtg cta aaa aga tgc ctt ctt cat ttg gct 50
Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala
1 5 10

gtg ata ggt gct ttg ctg gct gtg ggg gct aca aaa gta ccc aga aac 98
Val Ile Gly Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn
15 20 25

cag gac tgg ctt ggt gtc tca agg caa ctc aga acc aaa gcc tgg aac 146
Gln Asp Trp Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn
30 35 40 45

agg cag ctg tat cca gag tgg aca gaa gcc cag aga ctt gac tgc tgg 194
Arg Gln Leu Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp
50 55 60

aga ggt ggt caa gtg tcc ctc aag gtc agt aat gat ggg cct aca ctg 242
Arg Gly Gly Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu
65 70 75

att ggt gca aat gcc tcc ttc tct att gcc ttg aac ttc cct gga agc 290
Ile Gly Ala Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser
80 85 90

caa aag gta ttg cca gat ggg cag gtt atc tgg gtc aac aat acc atc 338
Gln Lys Val Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile
95 100 105

atc aat ggg agc cag gtg tgg gga gga cag cca gtg tat ccc cag gaa 386

202510"6224001

Ile Asn Gly Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu
 110 115 120 125
 act gac gat gcc tgc atc ttc cct gat ggt gga cct tgc cca tct ggc 434
 Thr Asp Asp Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly
 130 135 140
 tct tgg tct cag aag aga agc ttt gtt tat gtc tgg aag acc tgg ggc 482
 Ser Trp Ser Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly
 145 150 155
 caa tac tgg caa gtt cta ggg ggc cca gtg tct ggg ctg agc att ggg 530
 Gln Tyr Trp Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly
 160 165 170
 aca ggc agg gca atg ctg ggc aca cac acc atg gaa gtg act gtc tac 578
 Thr Gly Arg Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr
 175 180 185
 cat cgc cgg gga tcc cgg agc tat gtg cct ctt gct cat tcc agc tca 626
 His Arg Arg Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser
 190 195 200 205
 gcc ttc acc att act gac cag gtg cct ttc tcc gtg agc gtg tcc cag 674
 Ala Phe Thr Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln
 210 215 220
 ttg cgg gcc ttg gat gga ggg aac aag cac ttc ctg aga aat cag cct 722
 Leu Arg Ala Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro
 225 230 235
 ctg acc ttt gcc ctc cag ctc cat gac cct agt ggc tat ctg gct gaa 770
 Leu Thr Phe Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu
 240 245 250
 gct gac ctc tcc tac acc tgg gac ttt gga gac agt agt gga acc ctg 818
 Ala Asp Leu Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu
 255 260 265
 atc tct cgg gca cct gtg gtc act cat act tac ctg gag cct ggc cca 866
 Ile Ser Arg Ala Pro Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro
 270 275 280 285
 gtc act gcc cag gtg gtc ctg cag gct gcc att cct ctc acc tcc tgt 914
 Val Thr Ala Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys
 290 295 300
 ggc tcc tcc cca gtt cca ggc acc aca gat ggg cac agg cca act gca 962
 Gly Ser Ser Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala
 305 310 315
 gag gcc cct aac acc aca gct ggc caa gtg cct act aca gaa gtt gtg 1010
 Glu Ala Pro Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val
 320 325 330
 ggt act aca cct ggt cag gcg cca act gca gag ccc tct gga acc aca 1058
 Gly Thr Thr Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr
 335 340 345

10047539-011502
 202510-622400

tct gtc cag gtg cca acc act gaa gtc ata agc act gca cct gtg cag	1106
Ser Val Gln Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln	
350 355 360 365	
atg cca act gca gag agc aca ggt atg aca cct gag aag gtg cca gtt	1154
Met Pro Thr Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val	
370 375 380	
tca gag gtc atg ggt acc aca ctg gca gag atg tca act cca gag gct	1202
Ser Glu Val Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala	
385 390 395	
aca ggt atg aca cct gca gag gta tca att gtg gtg ctt tct gga acc	1250
Thr Gly Met Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr	
400 405 410	
aca gct gca cag gta aca act aca gag tgg gtg gag acc aca gct aga	1298
Thr Ala Ala Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg	
415 420 425	
gag cta cct atc cct gag cct gaa ggt cca gat gcc agc tca atc atg	1346
Glu Leu Pro Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met	
430 435 440 445	
tct acg gaa agt att aca ggt tcc ctg ggc ccc ctg ctg gat ggt aca	1394
Ser Thr Glu Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr	
450 455 460	
gcc acc tta agg ctg gtg aag aga caa gtc ccc ctg gat tgt gtt ctg	1442
Ala Thr Leu Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu	
465 470 475	
tat cga tat ggt tcc ttt tcc gtc acc ctg gac att gtc cag ggt att	1490
Tyr Arg Tyr Gly Ser Phe Ser Val Thr Thr Asp Ile Val Gln Gly Ile	
480 485 490	
gaa agt gcc gag atc ctg cag gct gtg cag tcc ggt gag ggg gat gca	1538
Glu Ser Ala Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala	
495 500 505	
ttt gag ctg act gtg tcc tgc caa ggc ggg ctg ccc aag gaa gcc tgc	1586
Phe Glu Leu Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys	
510 515 520 525	
atg gag atc tca tgc cca ggg tgc cag ccc cct gcc cag egg ctg tgc	1634
Met Glu Ile Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys	
530 535 540	
cag cct gtg cta ccc agc cca gcc tgc cag ctg gtt ctg cac cag ata	1682
Gln Pro Val Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile	
545 550 555	
ctg aag ggt ggc tgc ggg aca tac tgc ctc aat gtg tct ctg gct gat	1730
Leu Lys Gly Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp	
560 565 570	
acc aac agc ctg gca gtg gtc agc acc cag ctt atc atg cct gtg cct	1778
Thr Asn Ser Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Val Pro	
575 580 585	

ggg att ctt ctc aca ggt caa gaa gca ggc ctt ggg cag gtt cgg ctg 1826
 Gly Ile Leu Leu Thr Gly Gln Glu Ala Gly Leu Gly Gln Val Arg Leu
 590 595 600 605

atc gtg ggc atc ttg ctg gtg ttg atg gct gtg gtc ctt gca tct ctg 1874
 Ile Val Gly Ile Leu Leu Val Leu Met Ala Val Val Leu Ala Ser Leu
 610 615 620

ata tat agg cgc aga ctt atg aag caa gac ttc tcc gta ccc cag ttg 1922
 Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp Phe Ser Val Pro Gln Leu
 625 630 635

cca cat agc agc agt cac tgg ctg cgt cta ccc cgc atc ttc tgc tct 1970
 Pro His Ser Ser Ser His Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser
 640 645 650

tgt ccc att ggt gag aat agc ccc ctc ctc agt ggg cag cag gtc tga 2018
 Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln Gln Val
 655 660 665

gtactctcat atgatgctgt gattttcctg gagttgacag aaacacctat atttccccca 2078
 gtcttcctcg ggagactact attaactgaa ataaatactc agagcctgaa aaa 2131

<210> 4
 <211> 668
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala Val Ile Gly
 1 5 10 15
 Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp
 20 25 30
 Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu
 35 40 45
 Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly
 50 55 60
 Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala
 65 70 75 80
 Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val
 85 90 95
 Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly
 100 105 110
 Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp
 115 120 125
 Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser
 130 135 140

1007239-01508
 2007-03-23

Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp
 145 150 155 160
 Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg
 165 170 175
 Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg
 180 185 190
 Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr
 195 200 205
 Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala
 210 215 220
 Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe
 225 230 235 240
 Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu
 245 250 255
 Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg
 260 265 270
 Ala Pro Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala
 275 280 285
 Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser
 290 295 300
 Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro
 305 310 315 320
 Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr
 325 330 335
 Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln
 340 345 350
 Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr
 355 360 365
 Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val
 370 375 380
 Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met
 385 390 395 400
 Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala
 405 410 415
 Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro
 420 425 430
 Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu
 435 440 445
 Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu
 450 455 460

10047539.041502
 202510.0327007

Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr
 465 470 475 480
 Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala
 485 490 495
 Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu
 500 505 510
 Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile
 515 520 525
 Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val
 530 535 540
 Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly
 545 550 555 560
 Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser
 565 570 575
 Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Val Pro Gly Ile Leu
 580 585 590
 Leu Thr Gly Gln Glu Ala Gly Leu Gly Gln Val Arg Leu Ile Val Gly
 595 600 605
 Ile Leu Leu Val Leu Met Ala Val Val Leu Ala Ser Leu Ile Tyr Arg
 610 615 620
 Arg Arg Leu Met Lys Gln Asp Phe Ser Val Pro Gln Leu Pro His Ser
 625 630 635 640
 Ser Ser His Trp Leu Arg Leu Pro Arg Ile Phe Cys Ser Cys Pro Ile
 645 650 655
 Gly Glu Asn Ser Pro Leu Leu Ser Gly Gln Gln Val
 660 665

<210> 5
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 5
 Lys Thr Trp Gly Gln Tyr Trp Gln Val
 1 5

<210> 6
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 6

10047539.011502

Ile Thr Asp Gln Val Pro Phe Ser Val
1 5

<210> 7
<211> 10
<212> PRT
<213> Homo sapiens

<400> 7
Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val
1 5 10

<210> 8
<211> 9
<212> PRT
<213> Homo sapiens

<400> 8
Lys Thr Trp Gly Lys Tyr Trp Gln Val
1 5

<210> 9
<211> 10
<212> PRT
<213> Homo sapiens

<400> 9
Phe Leu Thr Pro Lys Lys Leu Gln Cys Val
1 5 10

<210> 10
<211> 9
<212> PRT
<213> Homo sapiens

<400> 10
Lys Leu Gln Cys Val Asp Leu His Val
1 5

<210> 11
<211> 10
<212> PRT
<213> Homo sapiens

<400> 11
Val Ile Ser Asn Asp Val Cys Ala Gln Val
1 5 10

10047539.014502

<210> 12
<211> 10
<212> PRT
<213> Homo sapiens

<400> 12
Gln Val His Pro Gln Lys Thr Val Thr Lys
1 5 10

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

<400> 13
His Leu Phe Gly Tyr Ser Trp Tyr Lys
1 5

10047539.011502